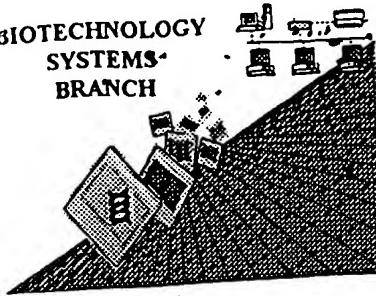


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1012

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/964 678
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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
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NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
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TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
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The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

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Checker Version 3.0 can be down loaded from the USPTO website at the following address:
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OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/964,678

DATE: 10/16/2001
TIME: 15:50:12

Input Set : A:\PTO.txt
Output Set: N:\CRF3\10162001\I964678.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: de la Monte, Suzanne
Wands, Jack R.
9 (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease

13 (iii) NUMBER OF SEQUENCES: 14

15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
17 (B) STREET: 1100 New York Ave., Suite 600
18 (C) CITY: Washington
19 (D) STATE: DC
20 (E) COUNTRY: USA
21 (F) ZIP: 20005-3934

(v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

29 (A) APPLICATION NUMBER: US/09/964,678 QV
C--> 30 (B) FILING DATE: 28-Sep-2001

C--> 31 (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

34 (A) NAME: Esmond, Robert W.
35 (B) REGISTRATION NUMBER: 32,893
36 (C) REFERENCE/DOCKET NUMBER: 0609.4370000

(ix) TELECOMMUNICATION INFORMATION:

39 (A) TELEPHONE: 202-371-2600
40 (B) TELEFAX: 202-371-2540

44 (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

46 (A) LENGTH: 1442 base pairs
47 (B) TYPE: nucleic acid
48 (C) STRANDEDNESS: double
49 (D) TOPOLOGY: both

52 (ii) MOLECULE TYPE: cDNA

55 (ix) FEATURE:
56 (A) NAME/KEY: CDS
57 (B) LOCATION: 15..1139

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

62 TTTTTTTTT TGAG ATG GAG TTT TCG CTC TTG CCC AGG CTG GAG TGC
Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys
63 1 5 10
64 AAT GGC GCA ATC TCA GCT CAC CGC AAC CTC CGC CTC CCG GGT TCA AGC
66 Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser
67 Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser

50

98

10/16/01

*Errored: Old Format
may only be used when
prior application date
preceded July 1, 1998*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/964,678

DATE: 10/16/2001
TIME: 15:50:12

Input Set : A:\PTO.txt
Output Set: N:\CRF3\10162001\I964678.raw

68	15	20	25		146
70	GAT TCT CCT GCC TCA GCC TCC CCA GTA GCT GGG ATT ACA GGC ATG TGC				
71	Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys				
72	30	35	40		194
74	ACC CAC GCT CGG CTA ATT TTG TAT TTT TTA GTA GAG ATG GAG TTT				
75	Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe				
76	45	50	55	60	242
78	CTC CAT GTT GGT CAG GCT GGT CTC GAA CTC CCG ACC TCA GAT GAT CCC				
79	Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro				
80	65	70	75		290
82	TCC GTC TCG GCC TCC CAA AGT GCT AGA TAC AGG ACT GGC CAC CAT GCC				
83	Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala				
84	80	85	90		338
86	CGG CTC TGC CTG GCT AAT TTT TGT GGT AGA AAC AGG GTT TCA CTG ATG				
87	Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met				
88	95	100	105		386
90	TGC CCA AGC TGG TCT CCT GAG CTC AAG CAG TCC ACC TGC CTC AGC CTC				
91	Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu				
92	110	115	120		434
94	CCA AAG TGC TGG GAT TAC AGG CGT GCA GCC GTG CCT GGC CTT TTT ATT				
95	Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile				
96	125	130	135	140	482
98	TTA TTT TTT TTA AGA CAC AGG TGT CCC ACT CTT ACC CAG GAT GAA GTG				
99	Leu Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val				
100	145	150	155		530
102	CAG TGG TGT GAT CAC AGC TCA CTG CAG CCT TCA ACT CCT GAG ATC AAG				
103	Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys				
104	160	165	170		578
106	CAT CCT CCT GCC TCA GCC TCC CAA GTA GCT GGG ACC AAA GAC ATG CAC				
107	His Pro Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His				
108	175	180	185		626
110	CAC TAC ACC TGG CTA ATT TTT ATT TTT ATT TTT AAT TTT TTG AGA CAG				
111	His Tyr Thr Trp Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln				
112	190	195	200		674
114	AGT CTC AAC TCT GTC ACC CAG GCT GGA GTG CAG TGG CGC AAT CTT GGC				
115	Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly				
117	205	210	215	220	722
119	TCA CTG CAA CCT CTG CCT CCC GGG TTC AAG TTA TTC TCC TGC CCC AGC				
120	Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser				
121	225.	230	235		770
123	CTC CTG AGT AGC TGG GAC TAC AGG CGC CCA CCA CGC CTA GCT AAT TTT				
124	Leu Leu Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe				
125	240	245	250		818
127	TTT GTA TTT TTA GTA GAG ATG GGG TTC ACC ATG TTC GCC AGG TTG ATC				
128	Phe Val Phe Leu Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile				
129	255	260	265		866
131	TTG ATC TCT GGA CCT TGT GAT CTG CCT GCC TCG GCC TCC CAA AGT GCT				
132	Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala				
133	270	275	280		

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/964,678

DATE: 10/16/2001
TIME: 15:50:12

Input Set : A:\PTO.txt
Output Set: N:\CRF3\10162001\I964678.raw

135	GGG ATT ACA GGC GTG AGC CAC CAC GCC CGG CTT ATT TTT AAT TTT TGT	914
136	Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys	
137	285 290 295 300	
139	TTG TTT GAA ATG GAA TCT CAC TCT GTT ACC CAG GCT GGA GTG CAA TGG	962
140	Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp	
141	305 310 315	
143	CCA AAT CTC GGC TCA CTG CAA CCT CTG CCT CCC GGG CTC AAG CGA TTC	1010
144	Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe	
145	320 325 330	
147	TCC TGT CTC AGC CTC CCA AGC TGG GAT TAC GGG CAC CTG CCA CCA	1058
148	Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro	
149	335 340 345	
151	CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT	1106
152	His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr	
153	350 355 360	
155	TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT	1159
156	Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg	
157	365 370 375	
159	TCCAAAGTGC TGGGATTACA GGCGTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA	1219
161	AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCAGGC TGGTCTCAA CTTCTGGCTT	1279
163	CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTAACAGTTACA	1339
165	TCTTTATTAGT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA	1399
167	GTAACAGAGT TCTTTATAA CTTTAAACA AAGCTTTAGA GCA	1442

170 (2) INFORMATION FOR SEQ ID NO: 2:

- 172 (i) SEQUENCE CHARACTERISTICS:
 - 173 (A) LENGTH: 375 amino acids
 - 175 (B) TYPE: amino acid
 - 176 (D) TOPOLOGY: linear

178 (ii) MOLECULE TYPE: protein

180	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
182	Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile	
183	1 5 10 15	
185	Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala	
186	20 25 30	
188	Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg	
189	35 40 45	
191	Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly	
192	50 55 60	
194	Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala	
195	65 70 75 80	
197	Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu	
198	85 90 95	
200	Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp	
201	100 105 110	
203	Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp	
204	115 120 125	
206	Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu	
207	130 135 140	
209	Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/964,678

DATE: 10/16/2001
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Input Set : A:\PTO.txt
Output Set: N:\CRF3\10162001\I964678.raw

210	145	150	155	160
212	His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala			
213	165	170	175	
215	Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp			
216	180	185	190	
218	Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser			
219	195	200	205	
221	Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro			
222	210	215	220	
224	Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser			
225	225	230	235	240
227	Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu			
228	245	250	255	
230	Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly			
231	260	265	270	
233	Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly			
234	275	280	285	
236	Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met			
237	290	295	300	
239	Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly			
240	305	310	315	320
242	Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser			
243	325	330	335	
245	Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn			
246	340	345	350	
248	Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp			
249	355	360	365	
251	Ser Gln Thr Pro Asp Leu Arg			
252	370	375		
254	(2) INFORMATION FOR SEQ ID NO: 3:			
256	(i) SEQUENCE CHARACTERISTICS:			
257	(A) LENGTH: 1381 base pairs			
258	(B) TYPE: nucleic acid			
259	(C) STRANDEDNESS: double			
260	(D) TOPOLOGY: both			
262	(ii) MOLECULE TYPE: cDNA			
267	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:			
269	TTTTTTTTT GAGATGGAGT TTTCGCTCTT GTGGCCCAAG CTGGAGTGCA ATGGCGCAAT		60	
271	CTCAGCTCAC CGCAACCTCC GCCTCCCCGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC		120	
273	AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTTTTAGTA		180	
275	GAGATGGAGT TTAACTCCAT GTGGTCTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC		240	
277	TCCCCTCTCG GCCTGCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCCTC		300	
279	TGCCTGGCTA ATTGGTGTGG TAGAACAGG GTTCACTGA TGTTGCCAA GCTGGTCTCC		360	
281	TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GGCAGTCAGCC		420	
283	GTGCCTGGCC TTTTATTTT ATTGAGACAGT GTACCACTCT TACCCAGGAT		480	
285	GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCCTGAGAT CAAGCAATCC		540	
287	TCCTGCTCA GCCTCCCAAG TAGCTGGAC CAAAGACATG CACCACTACA CCTGGTAATT		600	
289	TTTATTTTA TTTTAATTG TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC		660	
291	AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCCCTCCGG GTTCAAGTTA TTCTCCTGCC		720	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/964,678

DATE: 10/16/2001
TIME: 15:50:12

Input Set : A:\PTO.txt
Output Set: N:\CRF3\10162001\I964678.raw

293	CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCAAG CCTAGCTAAT TTTTTGTAT	780
295	TTTTAGTAGA GATGGGTTT CACCATGTTG GCCAGGTTGA TCTTGATCTC TTGACCTTGT	840
297	GATCTGCCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GTCTCGTACT CCACGCCGGC	900
299	CTATTTTAA TTTTTGTTTG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC	960
301	AATGGCAAAT CTCGGCTACT CGCAACCTCT GCCTCCCGGG TCAAGCGATT CTCCGTCTC	1020
303	AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTT	1080
305	CATTAGAGGC GGGTTTACCA TATTTGTCAG GCTGGGTCTC AAACCTCCTGA CCTCAGGTGA	1140
307	CCCACCTGCC TCAGCCTTCC AAAGTGCCTGG GATTACAGGC GTGAGGCCACC TCACCCAGCC	1200
309	GGCTAATTG GAATAAAAAA TATGTAGCAA TGGGGTCTG CTATGTTGCC CAGGCTGGTC	1260
311	TCAAACCTCT GGCTTCAGTC AATCCTCCA AATGAGCCAC AACACCCAGC CAGTCACATT	1320
313	TTTTAACAG TTACATCTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAA	1380
315	C	1381
317	(2) INFORMATION FOR SEQ ID NO: 4:	
319	(i) SEQUENCE CHARACTERISTICS:	
320	(A) LENGTH: 1418 base pairs	
321	(B) TYPE: nucleic acid	
322	(C) STRANDEDNESS: both	
323	(D) TOPOLOGY: both	
325	(ii) MOLECULE TYPE: cDNA	
330	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:	
332	TTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCCCAGG CTGGAGTGCA ATGGCGCAAT	60
334	CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCC CAGCCTCCCC	120
336	AGTAGGCTGG GATTACAGGC ATGTGCACCA CGCTCGGCTA ATTTGTATT TTTTTTAGT	180
338	AGAGATGGAG TTTCTCCATG TTGGTCAGGC TGGTCTCGAA CTCCGACCTC AGATGATCCT	240
340	CCCGTCTCGG CCTCCCAAAG TGCTAGATAC AGGACTGAGC ACCATGCCCG GCCTCTGCC	300
342	GGCTAATTG TGTGGTAGAA ACAGGGTTTC ACTGATGTGC CCAAGCTGGT CTCCGTAGCT	360
344	CAAGCAGTCC ACCTGCCTCA GCCTCCAAA GTGCTGGGAT TACAGCGTG CAGCGTGCC	420
346	TGGCCTTTT ATTATTTTT TTTTAAGACA CAGGTGTCCC ACTCTTACCC AGGATGAAGT	480
349	GCAGTGGGT GATCACAGCT CACTGCAGCC TTCAACTCTG AGATCAAGCA TCCCTCTGCC	540
351	TCAGCCTCCC AAAGTAGCTG GGACCAAAGA CATGCACAC TACACCTGGC TAATTTTAT	600
353	TTTTATTTT AATTTTTGA GACAGAGTCT CAACTCTGTC ACCCAGGCTG GAGTGCAGTG	660
355	GCGCAATCTT GGCTCACTGC AACCTCTGCC TCCCGGGTTC AAGTTATTCT CCTGCCCGAG	720
357	CCTCCTGAGT AGCTGGGACT ACAGGGGCC ACCACGCCCTA GCTAATTGTT TTGTTATTTT	780
359	AGTAGAGATG GGGTTTCACC ATGTTGCCA GGTGATGCT AGATCTCTG ACCTTGTGAT	840
361	CTGCCTGCC CGGCCTCCCA AAGTGCCTGGG ATTACAGGAC GTGACGCCA CGGCCCGGCC	900
363	TATTTTAAT TTTGTTGT TTGAAATGGA ATCTCACTCT GTTACCCAGG CTGGAGTGCA	960
365	ATGGCCAAAT CTGGCTCAC TGCAACCTCT GCCTCCCGGG CTCAAGCGAT TCTCCTGTCT	1020
367	CAGCCTCCCA AGCAGCTGGG ATTACGGCA CCTGCACCCAC ACCCCGCTAA TTTTTGTATT	1080
369	TTCATTAGAG GCGGGGTTTC ACCATATTG TCAGGCTGGT CTCAAACCTCC TGACCTCAGG	1140
371	TGACCCACCT GCCTCAGCT TCCAAAGTGC TGGGATTACA GGCCTGACGC CTACACCCAGC	1200
373	CGGCTAATT AGATAAAAAA ATATGTAGCA ATGGGGGGTC TTGCTATGTT GCCCAGGCTG	1260
375	GTCTCAAAC TCTGGCTCA TGCAATCCTT CCAAATGAGC CACAACACCC AGCCAGTCAC	1320
377	ATTTTAAAC AGTACATCT TTATTTAGT ATACTAGAAA GTGATACGAT AACATGGCGG	1380
379	AACCTGCAAAT TTGGAGTAGT ACAGAGTCTT TTATAACT	1418
381	(2) INFORMATION FOR SEQ ID NO: 5:	
383	(i) SEQUENCE CHARACTERISTICS:	
384	(A) LENGTH: 22 base pairs	
385	(B) TYPE: nucleic acid	
386	(C) STRANDEDNESS: single	

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/964,678

DATE: 10/16/2001

TIME: 15:50:13

Input Set : A:\PTO.txt

Output Set: N:\CRF3\10162001\I964678.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]